

SEQUENCE LISTING

<110> CHANG, Y-H
VETRO, J.A.
MICKA, W.S.

<120> Dominant Negative Variants of Methionine Aminopeptidase
2 ("MetAP2") and Clinical Uses Therefor

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<140>
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<170> PatentIn Ver. 2.0

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Lys Lys Lys Lys Lys Lys
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 Lys Lys Lys Ser Asn Val Lys Lys Ile
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Ser Ala Ala Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val
50 55 60

Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
65 70 75 80

Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Thr
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
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Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
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Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
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 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
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 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
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 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
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 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
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 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
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 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
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Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
35 40 45

Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
65 70 75 80

Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
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 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
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 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
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 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
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 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
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 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
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 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
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 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
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 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335
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 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
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Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
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							20	25					30		

Asp	Glu	Ser	Asp	Pro	Val	Glu	Ser	Lys	Lys	Lys	Asn	Lys	Lys	Lys	Lys
							35	40			45				

Lys	Lys	Lys	Ser	Asn	Val	Lys	Lys	Ile	Glu	Leu	Leu	Phe	Pro	Asp
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Gly	Lys	Tyr	Pro	Glu	Gly	Ala	Trp	Met	Asp	Tyr	His	Gln	Asp	Phe	Asn
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Leu	Gln	Arg	Thr	Thr	Asp	Glu	Glu	Ser	Arg	Tyr	Leu	Lys	Arg	Asp	Leu
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Glu	Arg	Ala	Glu	His	Trp	Asn	Asp	Val	Arg	Lys	Gly	Ala	Glu	Ile	His
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Arg	Arg	Val	Arg	Arg	Ala	Ile	Lys	Asp	Arg	Ile	Val	Pro	Gly	Met	Lys
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Leu	Met	Asp	Ile	Ala	Asp	Met	Ile	Glu	Asn	Thr	Thr	Arg	Lys	Tyr	Thr
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Gly	Ala	Glu	Asn	Leu	Leu	Ala	Met	Glu	Asp	Pro	Lys	Ser	Gln	Gly	Ile
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Gly	Xaa	Pro	Thr	Gly	Leu	Ser	Leu	Asn	His	Cys	Ala	Ala	Xaa	Phe	Thr
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Pro	Asn	Ala	Gly	Asp	Lys	Thr	Val	Leu	Lys	Tyr	Glu	Asp	Val	Met	Lys
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Val	Xaa	Tyr	Gly	Val	Gln	Val	Asn	Gly	Asn	Ile	Ile	Xaa	Ser	Ala	Phe
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							260		265		270				

Gly	Xaa	Ser	Ile	Ala	Pro	Tyr	Arg	Xaa	Xaa	Gly	Gly	Lys	Ser	Val	Pro
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Ile	Val	Lys	Asn	Gly	Asp	Thr	Thr	Lys	Met	Glu	Glu	Gly	Glu	His	Phe
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aagaAGAAGA agggcaAAAG ggctgtgtca gcagtcaac aagaACTTGA taaAGAATCC 180
ggagcCTTGG tggatGAAGT agcaAAACAG ctggagAGCC aagcACTGGA ggagaAGGAG 240
agagatgacG acgatGAAGA tggagatGGT gatgtGTATG gtgcAACTGG gaagaAGAAG 300
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cacttgttAA atgtcatCAA cgaaaACTTC ggtaccCTTg ccttctGCC aaggtGCTG 1260
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aaaaAGAAGA agaACAAGAA aaAGAAGAAG aAGAAAAGCA atgtGAAGAA gattGAATTAA 180
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gacagaATCG ttccTGGGAT gaagttaATG gatATCGT ACATGATCGA aaataCTACA 420
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ggtaacatCA ttGATTCTGC ctTTACTGTt tccttGATC cacaataCGA taacCTGCTA 660
gccGCTGtaA aggacGCTAC ttacacGGGT attaaAGAAAG CGGGTATCGA tGtGAGATT 720
accgacatCG gtGAAAGCCAT ccaAGAAAGTT atGAAATCCT acgaAGTGG AATCAATGGT 780
gagacttAcc aggttAAAGT ttGtGCTGAAT ctatGtGGCC acatGATCGC accatATCGT 840
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cgatacCTAG acagacttGG ccaAGAGAAA tacttattTG cgttGAATAA CTTGGTTAGA 1140
cacGGTTAG tacaggATTA tccaccATTG AACGATATCC CGGATCCTA CACTGCACAA 1200
ttcgaacaca ccatttGTT gcatGTCAC aaaaAGGAAG tcGTTcGAA AGGTGATGAC 1260
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 Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
 65 70 75 80
 Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
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 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
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 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
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 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
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 Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
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 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
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 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
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Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
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 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
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 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
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 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
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 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
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 65 70 75 80
 Arg Asp Asp Asp Asp Glu Asp Gly Asp Ala Asp Gly Ala Thr
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 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
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 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
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 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
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 Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
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 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
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 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
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Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
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Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
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Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
 85 90 95

Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
 100 105 110

Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
 115 120 125

Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Arg Lys Tyr Thr
 130 135 140

Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
 145 150 155 160

Gly Phe Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala His Phe Thr
 165 170 175

Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
 180 185 190

Val Asp Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Asp Ser Ala Phe
 195 200 205

Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
 210 215 220

Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
 225 230 235 240

Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
 245 250 255

Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Leu Cys
 260 265 270

Gly His Ser Ile Ala Pro Tyr Arg Ile His Gly Gly Lys Ser Val Pro
 275 280 285

Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
 290 295 300

Ala Ile Glu Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
 305 310 315 320

Gly Glu Val Ser His Tyr Ala Arg Ser Ala Glu Asp His Gln Val Met
 325 330 335

Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
 340 345 350

Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln
 355 360 365

Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
 370 375 380

Gln Asp Tyr Pro Pro Leu Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
 385 390 395 400

Phe Glu His Thr Ile Leu Leu His Ala His Lys Lys Glu Val Val Ser
 405 410 415

Lys Gly Asp Asp Tyr Gly Lys Met Arg Phe Gln Met Ala Ser Ser Leu
 420 425 430

Gly Ile Ile Leu Leu
 435

<210> 15

<211> 71

<212> PRT

<213> Rat polylysine

<400> 15

Lys	Lys	Lys	Arg	Arg	Lys	Lys	Lys	Gly	Lys	Gly	Ala	Val	Ser	Ala
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Gly	Gln	Gln	Glu	Leu	Asp	Lys	Glu	Ser	Gly	Thr	Ser	Val	Asp	Glu	Val
20						25						30			

Ala	Lys	Gln	Leu	Glu	Arg	Gln	Ala	Leu	Glu	Glu	Lys	Glu	Lys	Asp	Asp
35						40					45				

Asp	Asp	Glu	Asp	Gly	Asp	Gly	Asp	Gly	Ala	Ala	Gly	Lys	Lys		
50				55					60						

Lys															
65					70										

<210> 16

<211> 480

<212> PRT

<213> Rat dnvMetAP2

<220>

<221> SITE

<222> (219)

<223> May be any naturally occurring amino acid

<220>

<221> SITE

<222> (231)

<223> May be any amino acid, except His

<220>

<221> SITE

<222> (251)

<223> May be any naturally occurring amino acid

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<222> (262)

<223> May be any naturally occurring amino acid

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Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
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Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
 35 40 45

Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
 50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80

Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala
 85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
 100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Cys
 450 455 460
 Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
 465 470 475 480

<210> 17
 <211> 480

<212> PRT
<213> Rat MetAP2

<400> 17
Met Ala Gly Val Glu Glu Ala Ser Ser Phe Gly Gly His Leu Asn Arg
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Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
20 25 30
Glu Ala Ala Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
35 40 45
Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
50 55 60
Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
65 70 75 80
Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala
85 90 95
Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
100 105 110
Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125
Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140
Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160
Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175
Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190
Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205
Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
210 215 220
Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240
Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
245 250 255
Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
260 265 270
Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
275 280 285
Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
290 295 300
Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
305 310 315 320
Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Cys
 450 455 460
 Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
 465 470 475 480

<210> 18
 <211> 1944
 <212> DNA
 <213> Rat MetAP2 variant

 <220>
 <221> misc_feature
 <222> (779)
 <223> Any nucleotide

<400> 18
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 gccacctgaa tcgcgacctg gatccagacg acagggaaaga gggAACCTCC agcacggccg 180
 aggaagccgc caagaagaaa agacggaaga agaagaaggg caaaAGGGCT gtgtcagcag 240
 ggcacaacaaga acttgataaa gaatcgggaa cctcagtggaa cgaagttagca aaacagtgg 300
 agagacaacg actggaggag aaagagaaag atgatgacgaa tgaagatggaa gatggatgg 360
 gtgatggatgc agctggaaaga aagaagaaaa agaagaagaa gaagagagga ccaagagtcc 420
 aaacagaccc tccctcagggtt ccaatatgtg acctgtatcc taatgggtta tttcccaaag 480
 gacaagatgt tgaataccca cccacccaag atggcggac agctgcttgg agaaccacaa 540
 gtgaagagaa aaaggcgcta gaccaggcta gtgaggagat ttggaacacg ttccgagaag 600
 ctgccgaagc acaccggccaa gttagaaat acgtcatgag ctggatcaag cctggatgt 660
 caatgataga aatatgtgag aagtggaaag actgttcccg aaagctata aaggagaatg 720
 ggttaaatgc aggccctggcc ttccctactg ggtgttctct caacaactgt gctgcagcnt 780
 acactcccaa tgctgggtgac acgacagtct tacagttagca cgacatctgt aagatcgact 840
 ttggaaacgca tataagtgtt agaataatttgc atttgtctt tactgttact tttaatccca 900
 aatatgacat attattaaaa gctgtaaaag atGCCACCAA tactggata aagtgtcg 960
 ggattgacgt ccgtctctgt gatgtcgccg aggccattca agaagttagt gagtccatgt 1020
 aagtggaaat agatggaaag acctaccaag tggaaacccat acgttaactta aatggacatt 1080
 caattggcc atatagaatt catgctggaa aaacagtgcc cattgtggaa ggagggaaag 1140
 ctacaaggat ggaggaagga gaggtgtatg ccattgagac ctttggatgc acagggaaagg 1200
 gcgtggttca tgacgatatg gaatgttac actacatgaa aaattttgtatgttggacacg 1260
 tgccaataag gcttccaaga acaaaacact tggtaatgtt catcaatgaa aactttggta 1320
 cccttgcctt ctggccgaaagg tggctggatc gcttgggaga aagtaataac ttaatggctc 1380

tgaagaacct gtgtgacttg ggcattttag atccatatcc accactctgt gacatcaaag 1440
 gatcatacac agcacagttt gaacatacca tactctgcgc ccaacctgta aagaagtgt 1500
 cagcagagga gatgactatt aaaacttagt ccaaagccaa ctcaacgtct ttattttcta 1560
 agcttggta gaacacatta taccacaat aatttgcac atgtctgtt taacagtgg 1620
 cctgtgtaat gccgttatcc atgtttaaag gagtttgatc aaaggccaaac tgtctacatg 1680
 taattaacca aggaaaaggc tttcaagact ttactgttaa ctgtttctcc cgtctaggaa 1740
 atgctgtact gctcactagt taggaattac ttaaacgttt tggtttgaag acctaagaga 1800
 tgcttttgg atatttatat tgccatattc ttacttggat gctttgaatg actacatata 1860
 tccagttctg cacctatgcc ctctggatt gcttttaac ctccctggaa tccattttct 1920
 aaaaaataaaa gacattttca gatc 1944

<210> 19
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
transit peptide

<400> 19
Gly Arg Lys Lys Arg Arg Gln Arg
1 5

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 20
gcgcaagctt atgattgaat tactgtttcc agatggaaag 40

<210> 21
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 21
gcgcctcgag tcagtagtca tcaccttcg aaacg 35

<210> 22
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
peptide

<400> 22
Cys Lys Glu Val Val Ser Lys Gly Asp Asp Tyr
1 5 10

<210> 23
<211> 9
<212> PRT

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: synthetic peptide

<400> 23
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: synthetic peptide

<400> 24
Met Gly Met Met
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<210> 25
<211> 63
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 25
cacactcgac cgcgatgtac tactactact actactacta ctactacggg ccagatatac 60
gca 63

<210> 26
<211> 37
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 26
cacagaattc cccgcattttt cagcatgcct gctattt 37